SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Foerderung der Wissens

<120> Human semaphorin 6A-1 (SEMA6A-1), a novel gene involved
      in neuronal development and regeneration mechanisms
      during apoptosis, as a potential drug target structure

<130> 19592

<140>
<141>

<150> 98122441.3
<151> 1998-11-26

<160> 7

<170> PatentIn Ver. 2.1

<210> 1
<211> 3093
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(3093)

<400> 1
atg agg tca gaa gcc ttg ctg cta tat ttc aca ctg cta cac ttt gct   48
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
  1   5   10   15

ggg gct ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc   96
Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
              20   25   30

aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg   144
Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
          35   40   45

aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg   192
Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
      50   55   60

aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat   240
Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp

1

65	70	75	80

```
ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca    288
Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
                85                  90                  95

tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa    336
Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
            100                 105                 110

cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac    384
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
            115                 120                 125

gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc    432
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
            130                 135                 140

aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc    480
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145                 150                 155                 160

gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg    528
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
                165                 170                 175

ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc    576
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
            180                 185                 190

att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg    624
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
            195                 200                 205

acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa    672
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
            210                 215                 220

gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca    720
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225                 230                 235                 240

gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag    768
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
                245                 250                 255

gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag    816
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
```

```
                260                      265                      270

tgg acg tcg ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac    864
Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
        275                      280                      285

tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt    912
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
        290                      295                      300

atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac    960
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
305                      310                      315                      320

agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc   1008
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
                325                      330                      335

agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc   1056
Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
                340                      345                      350

tgg aca cca gtt cct gat gaa cga gtt cct aag ccc agg cca ggt tgc   1104
Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
        355                      360                      365

tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc   1152
Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
        370                      375                      380

cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag   1200
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
385                      390                      395                      400

gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc   1248
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
                405                      410                      415

aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat   1296
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
                420                      425                      430

cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg   1344
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
                435                      440                      445

aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt   1392
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
```

```
        450                        455                        460

ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat   1440
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465              470             475             480

gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc   1488
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
                485             490             495

agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt   1536
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
                500             505             510

ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc   1584
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
            515             520             525

aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat   1632
Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
            530             535             540

tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc   1680
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
545             550             555             560

aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat   1728
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
                565             570             575

ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg   1776
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
                580             585             590

gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat   1824
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
                595             600             605

ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc   1872
Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
            610             615             620

cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa   1920
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
625             630             635             640

ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc   1968
Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
```

                    645   650   655

ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc tac tgc   2016
Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
                    660   665   670

gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag   2064
Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
                    675   680   685

aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag   2112
Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
                    690   695   700

ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag   2160
Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705   710   715   720

gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc   2208
Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
                    725   730   735

aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg   2256
Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
                    740   745   750

acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg   2304
Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
                    755   760   765

aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc   2352
Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
                    770   775   780

aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc   2400
Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785   790   795   800

acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg   2448
Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
                    805   810   815

gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag   2496
Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
                    820   825   830

ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc   2544
Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala

```
             835                    840                    845

aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc    2592
Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
         850                    855                    860

aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc ccc aaa    2640
Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865                    870                    875                    880

gtt cca cag cgg gag gcc tcc ctg ggt ccc ccg gga gcc tcc ctg tct    2688
Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
                    885                    890                    895

cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac    2736
Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
                900                    905                    910

ggg gtt gac tat aag agg agc tac ccc acg aac tcg ctc acg aga agc    2784
Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
                915                    920                    925

cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc    2832
His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
         930                    935                    940

tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg    2880
Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945                    950                    955                    960

ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca    2928
Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
                    965                    970                    975

tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac gcc tac    2976
Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
                980                    985                    990

aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta aag ccg    3024
Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
                995                    1000                   1005

gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg aag    3072
Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
         1010                   1015                   1020

ccc aat gat gcg tgt aca taa                                        3093
Pro Asn Asp Ala Cys Thr
```

1025   1030

<210> 2
<211> 1030
<212> PRT
<213> Homo sapiens

<400> 2
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
  1   5   10   15

Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
               20   25   30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
               35   40   45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
           50   55   60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65   70   75   80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
               85   90   95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
               100   105   110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
  -            115   120   125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
               130   135   140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145   150   155   160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
                   165   170   175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
               180   185   190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
               195   200   205

```
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
    210                 215             220

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225                 230             235                 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
                245             250                 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
                260             265             270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
        275             280             285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
    290             295             300

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
305                 310             315                 320

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
                325             330             335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
            340             345             350

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
        355             360             365

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
    370             375             380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
385             390             395                 400

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
                405             410             415

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
            420             425             430

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
        435             440             445

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
    450             455             460
```

```
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465             470             475             480

Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
            485             490             495

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
            500             505             510

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
            515             520             525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
            530             535             540

Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
545             550             555             560

Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
            565             570             575

Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
            580             585             590

Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
            595             600             605

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
            610             615             620

His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
625             630             635             640

Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
            645             650             655

Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
            660             665             670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
            675             680             685

Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
            690             695             700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705             710             715             720
```

Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
                725   730   735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
            740   745   750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
            755   760   765

Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
    770   775   780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785   790   795   800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
            805   810   815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
            820   825   830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
            835   840   845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
    850   855   860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865   870   875   880

Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
-                   885   890   895

Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
            900   905   910

Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
            915   920   925

His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
    930   935   940

Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945   950   955   960

Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
            965   970   975

```
Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
        980                 985                 990

Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
        995                 1000                1005

Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
    1010                1015                1020

Pro Asn Asp Ala Cys Thr
025                 1030
```

<210> 3
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(216)

<400> 3
```
ccg ccg ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc    48
Pro Pro Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser
 1               5                  10                  15

cag cca tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac    96
Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
            20                  25                  30

gcc tac aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta   144
Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
            35                  40                  45

aag ccg gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc   192
Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
        50                  55                  60

atg aag ccc aat gat gcg tgt aca                                    216
Met Lys Pro Asn Asp Ala Cys Thr
    65                  70
```

<210> 4
<211> 72
<212> PRT

<213> Homo sapiens

<400> 4

```
Pro Pro Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser
 1               5                10                15


Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
             20                25                30


Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
         35                40                45


Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
         50                55                60


Met Lys Pro Asn Asp Ala Cys Thr
 65                  70
```

<210> 5
<211> 65
<212> PRT
<213> Homo sapiens

<400> 5

```
Pro Pro Pro Gln Pro Gln Arg Lys Pro Gln Val Gln Leu His Val Gln
 1               5                10                15


Pro Gln Ala Lys Pro His Val Gln Pro Gln Pro Val Ser Ser Ala Asn
             20                25                30


Thr Gln Pro Arg Gly Pro Leu Ser Gln Ala Pro Thr Pro Ala Pro Lys
         35                40                45


Phe Ala Pro Val Ala Pro Lys Phe Thr Pro Val Val Ser Lys Phe Ser
         50                55                60


Pro
 65
```

<210> 6
<211> 3862
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (658)..(3750)

<400> 6

```
ggcacgaggc tgcagccaac tccgctcccc gcgcactcgg ctgcccaggc gctcggaacc  60

cagcagcggc gctcctccgc ggtgccggtc gcccgcgatg cccgcttagc agcgtgtagc  120

agcggccagc atcaccacac ccgcggcacc gcgctgccgg ccgcagagcc gggccagagc  180

cttgcccccc tccccagcc cccaccccgc ccccgccct gaaatgactt gttaatcggc  240

gcagacacca ccaaggggac tcaccgaagt ggaatccaag tggaatttgg atttggagaa  300

gagtttcttg aacatttacc ctcttccttg ttggttttct ttttcttttt cttctttttt  360

tttttggctt cttttttcct ctccccttct ccgctcgtca ttggagatga acacatcgcg  420

tttgcatccc agaaagtagt cgccgcgact atttccccca aagagacaag cacacatgta  480

ggaatgacaa aggcttgcga aggagagagc cgcagccgcg gcccggagag atcccctcga  540

taatggatta ctaaatggga tacacgctgt accagttcgc tccgagcccc ggccgcctgt  600

ccgtcgatgc accgaaaagg gtgaagtaga gaaataaagt ctccccgctg aactact  657
```

```
atg agg tca gaa gcc ttg ctg cta tat ttc aca ctg cta cac ttt gct  705
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1               5                  10                 15

ggg gct ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc  753
Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
            20                 25                 30

aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg  801
Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
        35                 40                 45

aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg  849
Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
    50                 55                 60

aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat  897
Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
65                 70                 75                 80

ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca  945
```

13

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
                    85   90   95

tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa   993
Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
            100   105   110

cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac   1041
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
            115   120   125

gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc   1089
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
            130   135   140

aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc   1137
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145   150   155   160

gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg   1185
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
                165   170   175

ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc   1233
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
                180   185   190

att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg   1281
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
            195   200   205

acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa   1329
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
            210   215   220

gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca   1377
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225   230   235   240

gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag   1425
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
                245   250   255

gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag   1473
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
                260   265   270

tgg acg tcg ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac   1521

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
        275   280   285

tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt   1569
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
        290   295   300

atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac   1617
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
305   310   315   320

agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc   1665
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
                325   330   335

agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc   1713
Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
                340   345   350

tgg aca cca gtt cct gat gaa cga gtt cct aag ccc agg cca ggt tgc   1761
Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
                355   360   365

tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc   1809
Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
        370   375   380

cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag   1857
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
385   390   395   400

gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc   1905
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
                405   410   415

aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat   1953
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
                420   425   430

cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg   2001
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
                435   440   445

aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt   2049
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
        450   455   460

ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat   2097

```
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465             470             475             480


gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc    2145
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
                485             490             495


agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt    2193
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
                500             505             510


ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc    2241
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
        515             520             525


aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat    2289
Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
        530             535             540


tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc    2337
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
545             550             555             560


aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat    2385
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
                565             570             575


ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg    2433
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
                580             585             590


gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat    2481
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
        595             600             605


ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc    2529
Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
        610             615             620


cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa    2577
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
625             630             635             640


ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc    2625
Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
                645             650             655


ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc tac tgc    2673
```

```
                    Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
                                  660                 665                 670

gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag        2721
Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
              675                 680                 685

aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag        2769
Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
              690                 695                 700

ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag        2817
Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705                 710                 715                 720

gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc        2865
Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
                  725                 730                 735

aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg        2913
Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
                  740                 745                 750

acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg        2961
Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
                  755                 760                 765

aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc        3009
Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
                  770                 775                 780

aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc        3057
Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785                 790                 795                 800

acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg        3105
Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
                  805                 810                 815

gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag        3153
Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
                  820                 825                 830

ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc        3201
Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
                  835                 840                 845

aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc        3249
```

17

```
Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
    850                 855                 860
```

```
aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc ccc aaa    3297
Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865                 870                 875                 880
```

```
gtt cca cag cgg gag gcc tcc ctg ggt ccc ccg gga gcc tcc ctg tct    3345
Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
                    885                 890                 895
```

```
cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac    3393
Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
                900                 905                 910
```

```
ggg gtt gac tat aag agg agc tac ccc acg aac tcg ctc acg aga agc    3441
Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
            915                 920                 925
```

```
cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc    3489
His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
        930                 935                 940
```

```
tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg    3537
Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945                 950                 955                 960
```

```
ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca    3585
Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
                965                 970                 975
```

```
tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac gcc tac    3633
Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
                980                 985                 990
```

```
aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta aag ccg    3681
Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
                995                 1000                1005
```

```
gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg aag    3729
Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
        1010                1015                1020
```

```
ccc aat gat gcg tgt aca taa tcccaggggg aggggtcag gtgtcgaacc    3780
Pro Asn Asp Ala Cys Thr
1025                1030
```

```
agcaggcaag gcgaggtgcc cgctcagctc agcaaggttc tcaactgcct cgagtaccca 3840
```

ccagaccaag aaggcctgcg gc   3862

<210> 7
<211> 1030
<212> PRT
<213> Homo sapiens

<400> 7

```
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1               5                  10                  15

Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
                 20                  25                  30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
             35                  40                  45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
         50                  55                  60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65                  70                  75                  80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
                 85                  90                  95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
                100                 105                 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
            115                 120                 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
        130                 135                 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145                 150                 155                 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
                165                 170                 175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
                180                 185                 190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
            195                 200                 205
```

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
    210   215   220

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225   230   235   240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
                245   250   255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
                260   265   270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
        275   280   285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
    290   295   300

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
305   310   315   320

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
                325   330   335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
                340   345   350

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
        355   360   365

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
    370   375   380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
385   390   395   400

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
                405   410   415

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
            420   425   430

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
            435   440   445

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
    450   455   460

Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465   470   475   480

Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
            485   490   495

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
            500   505   510

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
            515   520   525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
            530   535   540

Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
545   550   555   560

Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
            565   570   575

Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
            580   585   590

Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
            595   600   605

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
            610   615   620

His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
625   630   635   640

Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
            645   650   655

Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
            660   665   670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
            675   680   685

Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
            690   695   700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705   710   715   720

Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
         725   730   735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
         740   745   750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
         755   760   765

Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
 770   775   780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785   790   795   800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
         805   810   815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
         820   825   830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
         835   840   845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
    850   855   860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865   870   875   880

Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
         885   890   895

Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
         900   905   910

Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
         915   920   925

His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
    930   935   940

Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945   950   955   960

Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
         965   970   975

```
Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
            980                 985             990


Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
        995                 1000                1005


Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
    1010                1015                1020


Pro Asn Asp Ala Cys Thr
025                 1030
```